

Docket No.: PF-0319-2 DIV
Inventors: Bandman et al.
Title: HUMAN PROTEIN PHOSPHATASE
Serial No.: To Be Assigned

9	18	27	36	45	54
5' NNA TAT TGT ACC TAT CAG GCG TCA GCT CTC AAT CTA GAT CCC TCC CTG GCC TCG					
63	72	81	90	99	108
GAC TTA TTG CAA AAC ATG GGT GCT TTT TTG GAT AAA CCC AAA ACT GAA AAA CAT	M G A F L D K P K T E K H				
117	126	135	144	153	162
AAT GCT CAT GGT GCT GGG AAT GGT TTA CGT TAT GGC CTG AGC AGC ATG CAA GGA	N A H G A G N G L R Y G G L S S M Q G				
171	180	189	198	207	216
TGG AGA GTG GAA ATG GAA GAT GCA CAC ACA GCT GTT GTA GGT ATT CCT CAC GGC	W R V E M E D A H T A V V G I P H G				
225	234	243	252	261	270
TTG GAA GAC TGG TCA TTT TTT TTT GCA GTT TAT GAT GGT CAT GCT GGA TCC CGA GTG	L E D W S F F A V Y D G H A G S R V				
279	288	297	306	315	324
GCA AAT TAC TGC TCA ACA CAT TTA TTA GAA CAC ATC ACT ACT AAC GAA GAC TTT	A N Y C S T H L L E H I T T N E D F				
333	342	351	360	369	378
AGG GCA GCT GGA AAA TCA GGA TCT GCT CTT GAG CTT TCA GTG GAA AAT GTT AAG	R A A G K S G S A L E L S V E N V K				

FIGURE 1A

387	396	405	414	423	432
AAT GGT ATC AGA ACT GGA TTT TTG AAA ATT GAT GAA TAC ATG CGT AAC TTT TCA					
N G I R T G G F L K I D E Y M R N F S					
441	450	459	468	477	486
GAC CTC AGA AAC GGG ATG GAC AGG AGT GGT TCA ACT GCA GTG GGA GTT ATG ATT					
D L R N G M D R S G S T A V G V M I					
495	504	513	522	531	540
TCA CCT AAG CAT ATC TAC TTT ATC AAC TGT GGT GAT TCA CGT GCT GTT CTG TAT					
S P K H I Y F I N C G D S R A V L Y					
549	558	567	576	585	594
AGG AAT GGA CAA GTC TGC TTT TCT ACC CAG GAT CAC AAA CCT TGC AAT CCA AGG					
R N G Q V C F S T Q D H K P C N P R					
603	612	621	630	639	648
GAA AAG GAG CGA ATC CAA AAT GCA GGA GGC AGC GTG ATG ATA CAA CGT GTT AAT					
E K E R I Q N A G G S S V M I Q R V N					
657	666	675	684	693	702
GGT TCA TTA GCA GTA TCT CGT GCT GGT GGC GAC TAT GAT TAC AAG TGT GTT GAT					
G S L A V S R A L G D Y D Y K C V D					
711	720	729	738	747	756
GGC AAG GGC CCA ACA GAA CAA CTT GTT TCT CCA GAG CCT GAG GTT TAT GAA ATT					
G K G P T E Q L V S P E P E V Y E I					

FIGURE 1B

765	774	783	792	801	810
TTA AGA GCA GAA GAG GAT GAA TTT ATC ATC TTG GCT TGT GAT GGG ATC TGG GAT					
L R A E E D E F I I I L A C D G I W D					
819	828	837	846	855	864
GTT ATG AGT AAT GAG GAG CTC TGT GAA TAT GTT AAA TCT AGG CTT GAG GTA TCT					
V M S N E E E L C E Y V K S R L E V S					
873	882	891	900	909	918
GAT GAC CTG GAA AAT GTG TGC AAT TGG GTA GTG GAC ACT TGT TTA CAC AAG GGA					
D D L E N V C N W V V D T C L H K G					
927	936	945	954	963	972
AGT CGA GAT AAC ATG AGT ATT GTA CTA GTT TGC TTT TCA AAT GCT CCC AAG GTC					
S R D N M S I V L V C F S N A P K V					
981	990	999	1008	1017	1026
TCA GAT GAA GCG GTG AAA AAA GAT TCA GAG TTG GAT AAG CAC TTG GAA TCA CGG					
S D E A V K K D S E L D K H L E S R					
1035	1044	1053	1062	1071	1080
GTT GAA GAG ATT ATG GAG AAG TCT GGC GAG GAA GGA ATG CCT GAT CTT GCC CAT					
V E E I M E K S G E E G M P D L A H					
1089	1098	1107	1116	1125	1134
GTC ATG CGC ATC TTG TCT GCA GAA AAT ATC CCA AAT TTG CCT CCT GGG GGA GGT					
V M R I L S A E N I P N L P P G G G					

FIGURE 1C

1143	1152	1161	1170	1179	1188
CTT GCT GGC AAG CGT AAT GTT ATT GAA GCT GTT TAT AGT AGA CTG AAT CCA CAT					
L A G K R N V I E A V Y S R L N P H					
1197	1206	1215	1224	1233	1242
AGA GAA AGT GAT GGG GCC TCC GAT GAA GCA GAG GAA AGT GGA TCA CAG GGA AAA					
R E S D G A S D E A E E S G S Q G K					
1251	1260	1269	1278	1287	1296
TTG GTG GAA GCT CTC AGG CAA ATG AGA ATT AAT CAT AGG GGA AAC TAC CGA CAA					
L V E A A L R Q M R I N H R G N Y R Q					
1305	1314	1323	1332	1341	1350
CTT CTG GAG GAG ATG CTG ACT AGT TAC AGG CTA GCT AAA GTA GAG GGA GAA GAA					
L L E E M L T S Y R L A K V E G E E					
1359	1368	1377	1386	1395	1404
AGC CCT GCT GAA CCA GCT GCC ACA GCT ACT TCT TCG AAC AGT GAT GCT GGA AAC					
S P A E P A A T A T S S N S D A G N					
1413	1422	1431	1440	1449	1458
CCA GTG ACA ATG CAG GAA AGC CAT ACT GAA TCA GAA AGT GGT CTT GCT GAA TTA					
P V T M Q E S H T E S E S G L A E L					
1467	1476	1485	1494	1503	1512
GAC AGC TCT AAT GAA GAT GCA GGG ACA AAG ATG AGT GGT GAA AAA ATA TGA CTT					
D S S N E D A G T K M S G E K I					

FIGURE 1D

1521	1530	1539	1548	1557	1566
TCC TTT TTG GTA ATA TTT TTG TGA TCT TTG ATG GTT TTT AAC CTA GGA AGT GTA					
1575	1584	1593	1602	1611	1620
ATG TAT GCA TTT ATA TAA CTG TTT TGT TAT TTG AAT CTT GGA AAA CTA GTT TTA					
1629	1638	1647	1656	1665	1674
TTA TAT TCA GAT AGC CTT GTT TTT TAA AAA GGC CTT TGC ATA CAC CTT TAT GAG					
1683	1692	1701	1710	1719	1728
ATA GTG TAA AAT TGA CTA TTT ATA GTA CTA TCG ATT TAA TGA AAT TAT ATG TCA					
1737	1746	1755	1764	1773	1782
TTT CAC ATT GTA TGC CAG AAA TTA GGC TAC CAA TTA TGA ATT AAA GTC AGT AGT					
1791	1800	1809	1818	1827	1836
TAA ATT AAT ACT AGA TAG AAT TAG AAA TTT TGA TTA GAG AGA TTA TGC TAT ATT					
1845	1854	1863	1872	1881	1890
ATG GAA AAA CTT GTT AAT GTA GAA TTA TAC TGC TTC ATA TTA TTT TAC CTA TTA					

FIGURE 1E

1899	1908	1917	1926	1935	1944
GTA CAC TCA TAG TTA GCT TTG TAA TAA ATT TAT GTT TTC TTT AAT AAT TTT AGT					
1953	1962	1971	1980	1989	1998
TCT TCA AAG AAT GGC TGA TGC TGG CCT GTA ATT TTT CTT TCA AGG ATG ATA ATT					
2007	2016	2025	2034	2043	2052
TGT GTG TTG TTT GAT TTG TTT ATA TTT TAC ATC TCT GTA GTT TTA TTT TTA GAA					
2061	2070	2079	2088	2097	2106
GTT GTG AGA TAT TGG ATG TGT GGC TAT TTT TCC TTT CTC TGT ATT CTT TAT GAA					
2115	2124	2133	2142	2151	2160
ACA TAA CTT TTG AAA AAC CTA TGT ATT ATT CAT ACA GCT TTG GTT TGT ATA TTC					
2169	2178	2187	2196	2205	2214
TGT ATA GCC TAA CTA CAC ACA TCA AAA TGT ATG TCA ACC AAG TGT TTA GAA TGA					
2223	2232	2241	2250	2259	2268
AAT TAT AAG TGT TTA AGT CCA AAT AAA GCA TGT GAT GTG GAA TAA TCA AAA AAA					

FIGURE 1F

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205020" DET2400T

AA 3'

FIGURE 1G

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1	M	G	A	F	L	D	K	P	K	T	E	K	H	N	A	H	G	A	G	N	G	L	R	Y	G	L	S	S	M	Q	G	W	R	V	E	M	E	D	A	H	13177
1	M	G	A	F	L	D	K	P	K	T	E	K	H	N	A	H	G	A	G	N	G	L	R	Y	G	L	S	S	M	Q	G	W	R	V	E	M	E	D	A	H	GI 247927
1	M	G	A	F	L	D	K	P	K	T	E	K	H	N	A	H	G	A	G	N	G	L	R	Y	G	L	S	S	M	Q	G	W	R	V	E	M	E	D	A	H	GI 452526
41	T	A	V	V	G	I	P	H	G	L	E	D	W	S	F	F	A	V	Y	D	G	H	A	G	S	R	V	A	N	Y	C	S	T	H	L	L	E	H	I	T	13177
41	T	A	V	V	G	I	P	H	G	L	E	D	W	S	F	F	A	V	Y	D	G	H	A	G	S	R	V	A	N	Y	C	S	T	H	L	L	E	H	I	T	GI 247927
41	T	A	V	V	G	I	P	H	G	L	D	N	W	S	F	F	A	V	Y	D	G	H	A	G	S	R	V	A	N	Y	C	S	T	H	L	L	E	H	I	T	GI 452526
81	T	N	E	D	F	R	A	A	G	K	S	G	S	A	L	E	L	S	V	E	N	V	K	N	G	I	R	T	G	F	L	K	I	D	E	Y	M	R	N	F	13177
81	T	N	E	D	F	R	A	A	D	K	S	G	S	A	L	E	P	S	V	E	N	V	K	T	G	I	R	T	G	F	L	K	I	D	E	Y	M	R	N	F	GI 247927
81	T	N	E	D	F	R	A	A	D	K	S	G	S	A	L	E	P	S	V	E	S	V	K	T	G	I	R	T	G	F	L	K	I	D	E	Y	M	R	N	F	GI 452526
121	S	D	L	R	N	G	M	D	R	S	G	S	T	A	V	G	V	M	I	S	P	K	H	I	Y	F	I	N	C	G	D	S	R	A	V	L	Y	R	N	G	13177
121	S	D	L	R	N	G	M	D	R	S	G	S	T	A	V	G	V	M	I	S	P	T	H	I	Y	F	I	N	C	G	D	S	R	A	V	L	C	R	N	G	GI 247927
121	S	D	L	R	N	G	M	D	R	S	G	S	T	A	V	G	V	M	V	S	P	T	H	M	Y	F	I	N	C	G	D	S	R	A	V	L	C	R	N	G	GI 452526
161	Q	V	C	F	S	T	Q	D	H	K	P	C	N	P	R	E	K	E	R	I	Q	N	A	G	G	S	V	M	I	Q	R	V	N	G	S	L	A	V	S	R	13177
161	Q	V	C	F	S	T	Q	D	H	K	P	C	N	P	M	E	K	E	R	I	Q	N	A	G	G	S	V	M	I	Q	R	V	N	G	S	L	A	V	S	R	GI 247927
161	Q	V	C	F	S	T	Q	D	H	K	P	C	N	P	V	E	K	E	R	I	Q	N	A	G	G	S	V	M	I	Q	R	V	N	G	S	L	A	V	S	R	GI 452526
201	A	L	G	D	Y	D	Y	K	C	V	D	G	K	G	P	T	E	Q	L	V	S	P	E	P	E	V	Y	E	I	L	R	A	E	E	D	E	F	I	I	L	13177
201	A	L	G	D	Y	D	Y	K	C	V	D	G	K	G	P	T	E	Q	L	V	S	P	E	P	E	V	Y	E	I	L	R	A	E	E	D	E	F	V	V	L	GI 247927
201	A	L	G	D	Y	D	Y	K	C	V	D	G	K	G	P	T	E	Q	L	V	S	P	E	P	E	V	Y	E	I	V	R	A	E	E	D	E	F	V	V	L	GI 452526

FIGURE 2A

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241	A	C	D	G	I	W	D	V	M	S	N	E	E	L	C	E	F	V	N	S	R	L	E	V	S	D	D	L	E	N	V	C	N	W	V	V	D	T	C	L	13177
241	A	C	D	G	I	W	D	V	M	S	N	E	E	L	C	E	F	V	N	S	R	L	E	V	S	D	D	L	E	N	V	C	N	W	V	V	D	T	C	L	GI 247927
241	A	C	D	G	I	W	D	V	M	S	N	E	E	L	C	E	F	V	K	S	R	L	E	V	S	D	D	L	E	N	V	C	N	W	V	V	D	T	C	L	GI 452526
281	H	K	G	S	R	D	N	M	S	I	V	L	V	C	F	S	N	A	P	K	V	S	D	E	A	V	K	K	D	S	E	L	D	K	H	L	E	S	R	V	13177
281	H	K	G	S	R	D	N	M	S	I	V	L	V	C	F	S	N	A	P	K	V	S	D	E	A	V	K	R	D	L	E	L	D	K	H	L	E	S	R	V	GI 247927
281	H	K	G	S	R	D	N	M	S	V	V	L	V	C	F	S	N	A	P	K	V	S	E	E	A	V	K	R	D	S	E	L	D	K	H	L	E	S	R	V	GI 452526
321	E	E	I	M	E	K	S	G	E	E	G	M	P	D	L	A	H	V	M	R	I	L	S	A	E	N	I	P	N	L	P	P	G	G	G	L	A	G	K	R	13177
321	E	E	I	M	Q	K	S	G	E	E	G	M	P	D	L	A	H	V	M	R	I	L	S	A	E	N	I	P	N	L	P	P	G	G	G	L	A	G	K	R	GI 247927
321	E	E	I	M	Q	K	S	G	E	E	G	M	P	D	L	A	H	V	M	R	I	L	S	A	E	N	I	P	N	L	P	P	G	G	G	L	A	G	K	R	GI 452526
361	N	V	I	E	A	V	Y	S	R	L	N	P	H	R	E	S	D	G	A	S	D	E	A	E	E	S	G	S	Q	G	K	L	V	E	A	L	R	Q	M	R	13177
361	N	V	I	E	A	V	Y	S	R	L	N	P	N	K	D	N	D	G	G	A	G	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 247927	
361	H	V	I	E	A	V	Y	S	R	L	N	P	H	K	D	N	D	G	G	A	G	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 452526	
401	I	N	H	R	G	N	Y	R	O	L	L	E	E	M	L	T	S	Y	R	L	A	K	V	E	G	E	S	P	A	E	P	A	A	T	A	T	S	S	N	13177	
383	-	-	-	-	-	-	-	-	-	-	L	E	D	S	L	V	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 247927	
383	-	-	-	-	-	-	-	-	-	-	L	E	D	S	L	V	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 452526	
441	S	D	A	G	N	P	V	T	M	Q	E	S	H	T	E	S	E	S	G	L	A	E	L	D	S	S	N	E	D	A	G	T	K	M	S	G	E	K	I	13177	
390	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 247927		
390	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 452526		

FIGURE 2B

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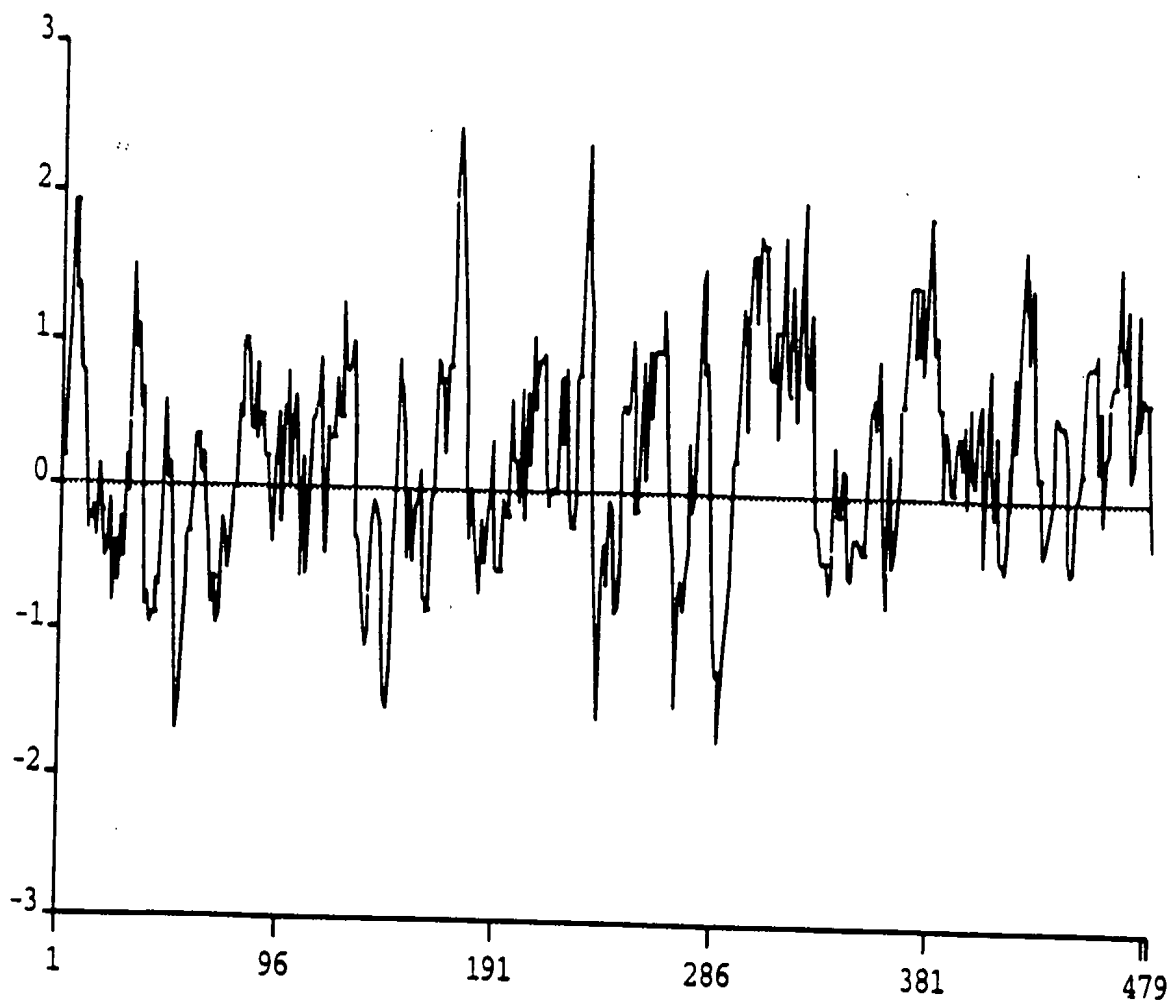
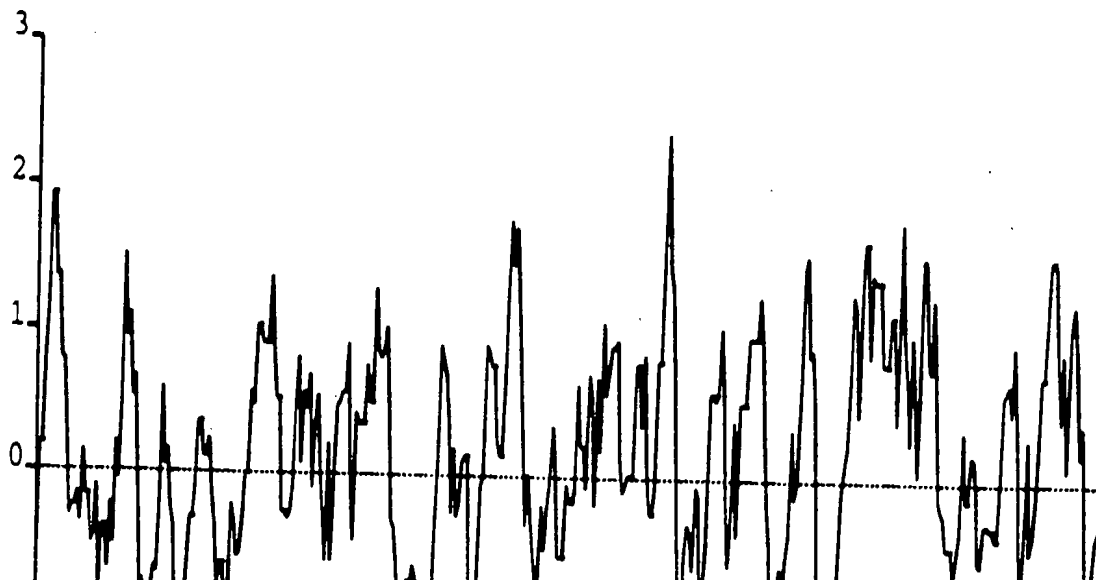


FIGURE 3A



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